

Figure S1. 48 hour supernatant from STYM1 contains inhibitory protein. A.) *P. gingivalis* end point growth after two days is shown with or without the addition of overnight or 48-hour supernatants from the STYM1 strain grown in BHI. Data represent the mean of three independent experiments and error bars represent one standard error about the mean. Statistical Significance was determined by One-way ANOVA (***) $p < 0.001$. B.) Shown is the pH of supernatant following the growth of the indicated *L. delbrueckii* strain after either 24 or 48 hrs. Data represent the mean of three independent experiments and error bars represent standard error. Statistical significance was determined by a two-way RM ANOVA (ns, not significant). C.) *P. gingivalis* end point growth after two days is shown with STYM1 supernatant or with STYM1 supernatant treated with either heat, proteinase K, or passage through a MWCO-filter. Data represent the mean of three independent experiments and error bars represent one standard

error about the mean. Statistical significance was determined by One-way ANOVA (***)
p<0.001).

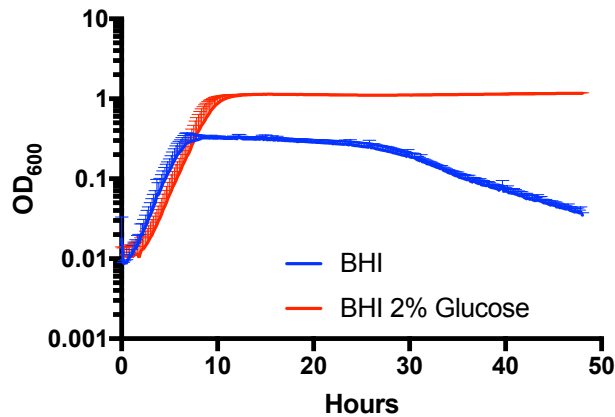
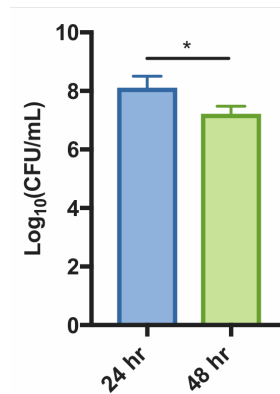
A**B**

Figure S2. STYM1 undergoes autolysis in late stationary phase due to carbon starvation.

A.) Growth curves of the STYM1 strain grown in either BHI or BHI supplemented with 2% glucose under anaerobic conditions. The growth curves represent the average of three independent experiments. Error bars represent the standard error. B.) Shown are the CFU/mL of the STYM1 strain at 24 hr and 48 hr of incubation in BHI medium. Data represent the average of three independent experiments and error bars represent the standard error about the mean. Statistical significance was determined by a student's t-test (*, $p < 0.05$).

Table S1. Proteins identified by mass spectrometry in 70kDa band of fraction 9 from gel filtration. Unique and total refer to the number of unique and total peptides identified for a given protein. The calculated molecular weight is also indicated.

Unique	Total	Protein	MWT(kDa)
59	260	Glutamine-fructose-6-phosphate aminotransferase	65.68
54	128	LBDND_1487 Pyruvate Oxidase	67.63
48	239	LBND_0761 Pyruvate Kinase	62.99
48	159	Phosphoenolpyruvate-protein phosphotransferase	63.04
47	130	Molecular Chaperone DnaK	66.02
43	162	CTP Synthetase	60.75
39	88	LDBND_1876 Oligopeptidase F, Metallopeptidase, MEROPS family	68.22
38	43	Preprotein translocase SecA	91.68
33	41	Threonine tRNA ligase	72.88
30	72	LDBND_0713 Trigger Factor	48.93
27	30	LDBND_1663 alpha-phosphoglucomutase	63.52
26	26	Aspartate tRNA ligase	69.43
25	44	Proline tRNA ligase	62.71
25	35	Asparagine synthetase B	75.52
24	33	Acylaminoacylpeptidase	73.92
22	22	LDBND_1525 60kDA Chaperonin groEL	57.29
22	22	LDBND_1569 1-deoxy-dxylulose-5-phosphate synthase 2	63.59
21	21	LDBND_1386 Xaa-Pro dipeptidase	88.36
20	23	LDBND_0509 Multicopper Oxidase	61.14
20	21	LDBND_0814 GTP pyrophosphokinase	84.9
18	18	GMP synthetase	57.34
17	23	LDBND_0712 Translation elongation factor tu	43.33
17	17	Mucus-binding Protein	116.15
17	17	Lysine tRNA ligase	58.31
16	16	LDBND_0412 Glutamyl-tRNA amidotransferase subunit A	51.79
16	16	Arginine tRNA ligase	64.13
14	14	ATP syntase subunit beta	52.12
14	14	Serine tRNA ligase	49.21
13	14	ATP-dependent Clp protease ATP-binding subunit	77.01
13	13	LDBND_1328 dihydroxyacetone kinase related enzyme	59.49
11	11	Clp Protease ClpE	81.7
11	11	LDBND_0571 Glyceraldehyde-3-phosphate dehydrogenase	36.56
10	10	elongation factor G	76.51
10	10	LDBND_2052 tRNA uridine-5-carboxymethylaminomethyl modification enzyme	70.48
9	9	Acetyl-CoA carboxylase biotin carboxylase	50.89
9	9	LBDND_0572 Phosphoglycerate kinase	42.7
9	9	LBDND_2030 Pyruvate/2-oxoglutarate dehydrogenase complex	48.46
9	9	Alanine tRNA ligase	97.42

9	9	LDBND_1705 6-phospho-alpha glucosidase	50.07
7	8	guanosine monophosphate reductase	40.1
7	8	LDBND_1752 Oxidoreductase	27.91
7	7	LDBND_1877 L-lactate oxidase	44.06
7	7	LDBND_1006 Carbamoyl-phosphate synthase large subunit	118.13
7	7	ATP synthase subunit alpha	54.63
6	6	LDBND_0970 HSDM-Type I modification subunit	60.2
6	6	LDBND_1769 Methyltransferase FkbM family	62.32
6	6	UDP-N-acetylmuramoyl-l-alanyl-D-glutamate-2,6-diaminopimelate ligase	56.78
6	6	LDBND_0069 Ribonucleotide reductase alpha	81.93
5	5	LDBND_0413 apartyl/glutamyl-rRNA amidotransferase	53.54
5	5	LDBND_1489 Pyruvate, water dikinase	89.57
5	5	LDBND_0696 Rnase J family beta-CASP ribonuclease	61.68
5	5	UMP Kinase	25.88
4	5	Succinate-semialdehyde dehydrogenase	50.23
4	5	Bifunctional N-Acetylglucosamine-1-phosphate uridyltransferase	49.83
4	5	LDBND_1287 Elongation factor Ts	37.36
4	4	LDBND_1925 FAD/FMN-containing dehydrogenase	51.78
4	4	LDBND_0778 Transcriptional regulator LysR family	35.65
4	4	Alpha-glycosidase	64.97
4	4	LDBND_0588 Phosphoglucosamine mutase	48.83
4	4	ribonucleoside-triphosphate reductase	83.59
4	4	PTS sucrose Transporter IIABC	68.274
4	4	LDBND_0088 Glucokinase	32.56
3	3	ATP-dependent Clp Protease ClpX	46.39
3	3	LDBND_1886 Fusion of IIA, IIB, and IIC component mannitol fructose phosphotransferase	69.59
3	3	LDBND_0208 Oligopeptidase O2	71.92
3	3	Class II fumarate hydratase	50.87
3	3	Isoleucine tRNA ligase	105.94
3	3	LDBND_1990 Hypothetical protein LDBND_1990(probable restriction endonuclease)	100.87
3	3	LDBND_1309 DNA/RNA helicase	133.07
3	3	LDBND_1999 Cation Transporting P-type ATPase	59.06
3	3	LDBND_0773 SSU ribosomal protein S1P	44.23
2	3	Hypothetical protein LDBND_0981	68.38
2	2	DNA directed RNA polymerase beta	135.4
2	2	Cell Division Protein FtsH	76.625
2	2	Acetyl-CoA carboxylase biotin carboxyl carrier protein	169.43
2	2	LDBND_1408 Glutamine synthetase	50.16
2	2	Cytochrome C	49.3
2	2	LDBND_1991 DNA recognition and methylase subunit Mod	62.13
2	2	LDBND_1143 Putative Phosphotransferase	32.1

2	2	D-Ala-D-Ala ligase A	40.14
2	2	LBDND_0477 Phosphoketolase	90.86
2	2	LBDND_0080 Butyryl-CoA dehydrogenase	57.39
2	2	Xaa-Pro dipeptidase	41.05
2	2	LBDND_0269 Predicted ATP-grasp enzyme	48.85
1	1	MutS Mismatch repair	87.46
1	1	LBDND_0789 Agrininosuccinate lyase	51.54
1	1	Nif3-like dinuclear metal center hexameric protein	29.2
1	1	LBDND_1445 DNA pol I	99.9
1	1	LBDND_0312 Ribosome-associated heat shock protein	8.93
1	1	LBDND_0823 Acyl carrier protein	9.12
1	1	LBDND_1931 Aminopeptidase N	95.27
1	1	Hypothetical protein	29.81
1	1	Hypothetical protein LDBND_2048	21.57
1	1	LBDND_0728 ABC Transporter ATP Binding Protein	38.373
1	1	LBDND_1872 ATPase component of ABC transporter	57.73
